

PAGE: 1  
*PRI 6865***RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/790,043A**DATE: 10/22/97  
TIME: 12:56:35**INPUT SET: S21089.raw**

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

#7/7R  
07/04/981                   **SEQUENCE LISTING**  
2  
3       (1)      General Information  
4  
5        (i) APPLICANT: Lonsdale, John  
6                   Milner, Peter  
7                   Payne, David  
8                   Pearson, Stewart  
9  
10      (ii) TITLE OF THE INVENTION: Novel FabI  
11  
12      (iii) NUMBER OF SEQUENCES: 2  
13  
14      (iv) CORRESPONDENCE ADDRESS:  
15        (A) ADDRESSEE: SmithKline Beecham Corporation  
16        (B) STREET: 709 Swedeland Road  
17        (C) CITY: King of Prussia  
18        (D) STATE: PA  
19        (E) COUNTRY: USA  
20        (F) ZIP: 19406-0939  
21  
22      (v) COMPUTER READABLE FORM:  
23        (A) MEDIUM TYPE: Diskette  
24        (B) COMPUTER: IBM Compatible  
25        (C) OPERATING SYSTEM: DOS  
26        (D) SOFTWARE: FastSEQ for Windows Version 2.0  
27  
28      (vi) CURRENT APPLICATION DATA:  
29        (A) APPLICATION NUMBER:  
30        (B) FILING DATE: 28-August-1997  
31        (C) CLASSIFICATION:  
32  
33      (vii) PRIOR APPLICATION DATA:  
34        (A) APPLICATION NUMBER: 60/024845  
35        (B) FILING DATE: 28-AUG-1996  
36  
37      (viii) ATTORNEY/AGENT INFORMATION:  
38        (A) NAME: Gimmi, Edward R  
39        (B) REGISTRATION NUMBER: 38,891  
40        (C) REFERENCE/DOCKET NUMBER: GM50005  
41  
42      (ix) TELECOMMUNICATION INFORMATION:  
43        (A) TELEPHONE: 610-270-4478  
44        (B) TELEFAX: 610-270-5090  
45        (C) TELEX:  
46**ENTERED**

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/790,043ADATE: 10/22/97  
TIME: 12:56:37

INPUT SET: S21089.raw

47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 256 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: protein

56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58

59 Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn  
60 1 5 10 15  
61 Lys Arg Ser Ile Ala Phe Gly Val Ala Lys Val Leu Asp Gln Leu Gly  
62 20 25 30  
63 Ala Lys Leu Val Phe Thr Tyr Arg Lys Glu Arg Ser Arg Lys Glu Leu  
64 35 40 45  
65 Glu Lys Leu Leu Glu Gln Leu Asn Gln Pro Glu Ala His Leu Tyr Gln  
66 50 55 60  
67 Ile Asp Val Gln Ser Asp Glu Glu Val Ile Asn Gly Phe Glu Gln Ile  
68 65 70 75 80  
69 Gly Lys Asp Val Gly Asn Ile Asp Gly Val Tyr His Ser Ile Ala Phe  
70 85 90 95  
71 Ala Asn Met Glu Asp Leu Arg Gly Arg Phe Ser Glu Thr Ser Arg Glu  
72 100 105 110  
73 Gly Phe Leu Leu Ala Gln Asp Ile Ser Ser Tyr Ser Leu Thr Ile Val  
74 115 120 125  
75 Ala His Glu Ala Lys Lys Leu Met Pro Glu Gly Gly Ser Ile Val Ala  
76 130 135 140  
77 Thr Thr Tyr Leu Gly Gly Glu Phe Ala Val Gln Asn Tyr Asn Val Met  
78 145 150 155 160  
79 Gly Val Ala Lys Ala Ser Leu Glu Ala Asn Val Lys Tyr Leu Ala Leu  
80 165 170 175  
81 Asp Leu Gly Pro Asp Asn Ile Arg Val Asn Ala Ile Ser Ala Gly Pro  
82 180 185 190  
83 Ile Arg Thr Leu Ser Ala Lys Gly Val Gly Gly Phe Asn Thr Ile Leu  
84 195 200 205  
85 Lys Glu Ile Glu Glu Arg Ala Pro Leu Lys Arg Asn Val Asp Gln Val  
86 210 215 220  
87 Glu Val Gly Lys Thr Ala Ala Tyr Leu Leu Ser Asp Leu Ser Ser Gly  
88 225 230 235 240  
89 Val Thr Gly Glu Asn Ile His Val Asp Ser Gly Phe His Ala Ile Lys  
90 245 250 255  
91

92

(2) INFORMATION FOR SEQ ID NO:2:

93

94 (i) SEQUENCE CHARACTERISTICS:

95 (A) LENGTH: 771 base pairs

96 (B) TYPE: nucleic acid

97 (C) STRANDEDNESS: double

98 (D) TOPOLOGY: linear

99

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PATENT APPLICATION US/08/790,043ADATE: 10/22/97  
TIME: 12:56:39

INPUT SET: S21089.raw

100                   (ii) MOLECULE TYPE: Genomic DNA  
101  
102                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
103  
104 ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGAA TCGCTAATAA GCGTAGTATT       60  
105 GCTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT       120  
106 AAAGAACGTA GCCGTAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAACG       180  
107 CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTT TGAGCAAATT       240  
108 GGTAAAGATG TTGGCAATAT TGATGGTGTAT TATCATTCAA TCGCATTGC TAATATGGAA       300  
109 GACCTACGCG GACGCTTTTC TGAAACTTCA CGTGAAGGCT TCTTGTAGC TCAAGACATT       360  
110 AGTTCTTACT CATTAAACAAT TGTGGCTCAT GAAGCTAAAA AATTAAATGCC AGAAGGTGGT       420  
111 AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAAATTA TAATGTGATG       480  
112 GGTGTTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCCT       540  
113 GATAATATTC GCGTTAATGC AATTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT       600  
114 GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC       660  
115 GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTRT TAAGTGACTT ATCAAGTGGC       720  
116 GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A       771  
117  
118

PAGE: 1

**SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/08/790,043A**

DATE: 10/22/97  
TIME: 12:56:40

***INPUT SET: S21089.raw***

Line

Error

Original Text